

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2001, 12:07:03 ; Search time 22.69 Seconds

(Without alignments)
1830.929 Million cell updates/sec

Title: US-09-486-334-2

Perfect score: 1641

Sequence: 1 MATCTDTCRTGNTGDDSRF.....IPCLTMQSTYLEMEDYVI 314

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 segs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organellar:*
9: SP-phage:*
10: SP-plant:*
11: SP-protist:*
12: SP-unclassified:*
13: SP-vertebrate:*
14: SP-virus:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1641	100.0	314	10	043297 arabidopsis
2	1611	98.2	314	10	042588 arabidopsis
3	1215	74.0	391	10	042532 arabidopsis
4	1208	73.6	336	10	039218 arabidopsis
5	877	53.4	347	10	093544 arabidopsis
6	872	53.1	289	10	09MA23 arabidopsis
7	869	53.0	294	10	039533 arabidopsis
8	861	52.5	289	10	09SDP2 arabidopsis
9	849.5	51.8	312	10	042538 arabidopsis
10	711	43.3	323	10	09ZP74 arabidopsis
11	699	42.5	368	10	09SIB0 arabidopsis
12	649.5	39.5	315	10	09SE76 arabidopsis
13	647.5	39.5	272	2	09JRH6 neisseria m
14	629.5	38.4	273	2	09KNT2 vibrio chol
15	610.5	37.2	402	10	09SLZ8 cyandiosch
16	587.5	35.8	299	10	09L3R1 rhizobium 1
17	587.5	35.8	299	10	081795 arabidopsis
18	472.5	28.8	270	3	09US33 schizosacch
19	422.5	25.7	227	2	032979 mycobacteri

20	415.5	25.3	245	2	086162	086162 synechococ
21	409	24.9	251	2	069218	069218 azotobacter
22	405	24.7	229	2	P95231	P95231 mycobacteri
23	395	24.1	229	2	09KGF5	09KGF5 bacillus ha
24	392	23.9	258	2	09HX16	09HX16 pseudomonas
25	391	23.8	243	1	09HNA4	09HNA4 methanosarc
26	388.5	23.7	212	2	09PPE6	09PPE6 campylobact
27	378	23.0	191	2	09LAR1	09LAR1 clostridium
28	370	22.5	265	2	044541	044541 azotobacter
29	338.5	20.6	220	2	09WZD4	09WZD4 thermotoga
30	312	19.0	171	1	09HPR3	09HPR3 halobacteri
31	307.5	18.7	305	5	09U8X2	09U8X2 entamoeba h
32	298	18.2	439	10	09MRF2	09MRF2 arabidopsis
33	290	17.7	300	5	09U8X0	09U8X0 entamoeba d
34	287	17.5	305	5	09U8X1	09U8X1 entamoeba d
35	265	16.1	231	1	09I210	09I210 pseudomonas
36	213	13.0	162	2	09F7A9	09F7A9 salmonella
37	207	12.6	184	2	09KTI3	09KTI3 vibrio chol
38	204	12.4	197	2	09S138	09S138 escherichia
39	193	11.8	275	5	09GV13	09GV13 leishmania
40	184.5	11.2	419	2	09RDX7	09RDX7 legionella
41	177.5	10.8	143	2	09KTH9	09KTH9 vibrio chol
42	175	10.7	236	2	09X1K7	09X1K7 thermotoga
43	175	10.7	246	2	09K9H8	09K9H8 bacillus ha
44	168	10.2	172	2	09X4C2	09X4C2 escherichia
45	162.5	9.9	239	2	09EZ10	09EZ10 staphylococ

ALIGNMENTS

RESULT 1
ID 043297 PRELIMINARY; PRT: 314 AA.
AC 043297;
DT 01-NOV-1996 (TREMURel. 01, Created)
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
DT 01-OCT-2000 (TREMURel. 15, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)
OS (114116.18).
OC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SOURCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=95154333; PubMed=7851429;
RA Ruffet M.L., Lebun M., Droux M., Douce R.;
RT "Subcellular distribution of serine acetyltransferase from Pisum
RT sativum and characterization of an Arabidopsis thaliana putative
RT cytosolic isoform".
RL Eur. J. Biochem. 227:500-509(1995).
RN [2]
RP SOURCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Ruffet M.L., Lebun M., Droux M., Douce R.;
RT Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SOURCE FROM N.A.
RC STRAIN=COLUMBIA;
RX Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altati H., Bel O., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thayer A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome
RT I.". J. Biol. Chem. 272:10000-10006(1997).
RN [4]
RP Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SOURCE FROM N.A.

RA Ecker J.R.;
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 Khan S., Kim C., Altali H., Bei B., Chin C., Chou J., Choi E.,
 Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
 Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 Thayer A., Tortumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 Theologis A., Ecker J.;
 RA Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 RL -i- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = CoA + O-ACETYL-L-
 CC SERINE.
 CC EMBL: Z34888; CAA84371.1; -
 DR EMBL: L34076; AAA58608.1; -
 DR EMBL: NC002304; AAF79319.1; -
 DR Mendel: 6700; Arath:1221;6701.
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep. 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 DR Transferrase; Acyltransferase.
 KM SEQUENCE 314 AA; 34251 MW; 78FACE3DA5CE04B0 CRC64;
 SQ

Query Match 100.0%; Score 1641; DB 10; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2,5e-125;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATCIDTCRTGNTODDSSRFCCIKNFRPGFSVNRKIHHTOIEDDDVWIKMLEAKSDV 60
 DB 1 MATCIDTCRTGNTODDSSRFCCIKNFRPGFSVNRKIHHTOIEDDDVWIKMLEAKSDV 60
 QY 61 KOEPLSNYYASTSHRSLESALAHILSVKLSNLPSTNLFELFISVLESPETIEST 120
 DB 61 KOEPLSNYYASTSHRSLESALAHILSVKLSNLPSTNLFELFISVLESPETIEST 120
 QY 121 KODLIANKERDPACISVHCFGLKGFACQAHRIAHITLMKONRKIVALLIONRVSESPA 180
 DB 121 KODLIANKERDPACISVHCFGLKGFACQAHRIAHITLMKONRKIVALLIONRVSESPA 180
 QY 181 VDIHPGAKIGKILLDHATGVIGETAVGDNVSIILHGVTLGSGTGOSGDRHPKIGDGL 240
 DB 181 VDIHPGAKIGKILLDHATGVIGETAVGDNVSIILHGVTLGSGTGOSGDRHPKIGDGL 240
 QY 241 IGAGSCILGNTTIGGAKIGSGSVVVDVPAKRTAVGNPARKLGKKNPKHDKIPCLTM 300
 DB 241 IGAGSCILGNTTIGGAKIGSGSVVVDVPAKRTAVGNPARKLGKKNPKHDKIPCLTM 300
 QY 301 DOTSYLEMSDYVI 314
 DB 301 DOTSYLEMSDYVI 314

RESULT 2
 Q42588 PRELIMINARY: PRT; 314 AA.

AC Q42588;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)

DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Murillo M., Foglia R., Diller A., Leustek T.;
 RL Cell Mol. Biol. Res. 0:0-0(0).
 CC -i- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = CoA + O-ACETYL-L-
 CC SERINE.
 CC EMBL: L42212; AAC37474.1; -
 DR Mendel: 6700; Arath:1221;6700.
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep. 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 DR Transferrase; Acyltransferase.
 KM SEQUENCE 314 AA; 34259 MW; A096DF6D2768E21C CRC64;
 SQ

Query Match 98.2%; Score 1611; DB 10; Length 314;
 Best Local Similarity 98.1%; Pred. No. 6.9e-123;
 Matches 308; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATCIDTCRTGNTODDSSRFCCIKNFRPGFSVNRKIHHTOIEDDDVWIKMLEAKSDV 60
 DB 1 MATCIDTCRTGNTODDSSRFCCIKNFRPGFSVNRKIHHTOIEDDDVWIKMLEAKSDV 60
 QY 61 KOEPLSNYYASTSHRSLESALAHILSVKLSNLPSTNLFELFISVLESPETIEST 120
 DB 61 KOEPLSNYYASTSHRSLESALAHILSVKLSNLPSTNLFELFISVLESPETIEST 120
 QY 121 KODLIANKERDPACISVHCFGLKGFACQAHRIAHITLMKONRKIVALLIONRVSESPA 180
 DB 121 KODLIANKERDPACISVHCFGLKGFACQAHRIAHITLMKONRKIVALLIONRVSESPA 180
 QY 181 VDIHPGAKIGKILLDHATGVIGETAVGDNVSIILHGVTLGSGTGOSGDRHPKIGDGL 240
 DB 181 VDIHPGAKIGKILLDHATGVIGETAVGDNVSIILHGVTLGSGTGOSGDRHPKIGDGL 240
 QY 241 IGAGSCILGNTTIGGAKIGSGSVVVDVPAKRTAVGNPARKLGKKNPKHDKIPCLTM 300
 DB 241 IGAGSCILGNTTIGGAKIGSGSVVVDVPAKRTAVGNPARKLGKKNPKHDKIPCLTM 300
 QY 301 DOTSYLEMSDYVI 314
 DB 301 DOTSYLEMSDYVI 314

RESULT 3
 Q42532 PRELIMINARY: PRT; 391 AA.

AC Q42532;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE).
 DE (SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SARI PRECURSOR).
 GN SAT-1 OR SAT A.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA MEDLINE=96270381; PubMed=8639741;
 RA Roberts M.A., Wray J.L.;
 RT "Cloning and characterization of an Arabidopsis thaliana cDNA clone encoding an organellar isoform of serine acetyltransferase.";

DR EMBL: D88530; BAA13635.1; -
 DR EMBL: D88529; BAA13634.1; -
 DR Mendei; 10792; Spio1.1221;10792.
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 KW Transferrase.
 SO SEQUENCE 347 AA; 37256 MW; FRAB365488DB6B0E CRC64;

Query Match 53.4%; Score 877; DB 10; Length 347;
 Best Local Similarity 56.6%; Pred. No. 2.9e-63;
 Matches 163; Conservative 53; Mismatches 70; Indels 2; Gaps 1;

QY 29 PG-FSVNKRHHHTQIEDDDVWIKMEAKSDVKOEPIISNTYYASITSHRSLSALAH 86
 DB 60 PGDLSVAPSVGHLTANNEAWLMQIKGEARDSEPALASLYSTLSSLSLSP 119
 QY 87 ILTVLSNMLPSNTLEFISVLESEPEITESTKODLIAVERDPACISYVHCFEGFG 146
 DB 120 HLGKLCSTLSTLLDLEFINLSSDSSLIDAVVADLRAARVRDPACVSHCLNKG 179
 QY 147 FLACQARIATLTKONKRIYALIONRSESPAVDHPKAGIKGILLDHTGVIGET 206
 DB 180 FLACQSHVAKHKNQRRPLALHSRISDVAVDHPKAGIKGILLDHTGVIGET 239
 QY 207 AVGDNVSTLHGVTLGCTGKSGDRHPKIGDGVLIAGSCILGNTITGSAKIGSGVYV 266
 DB 240 AITDNCSTLHHTVLTGCTGKAGDRHPKVGDLVIGAGATILGNVAGIKGAGSVYL 299
 QY 267 KDVPARTAVGNPARIIGKGNPKRHKIPCLMDQTSYLETMSDYVI 314
 DB 300 IDVPRTTAVGNPARIIGKGNPKRHKIPCLMDQTSYLETMSDYVI 347

RESULT 6
 O9MAZ3 PRELIMINARY; PRT; 289 AA.
 AC O9MAZ3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE SERINE ACETYLTANSFERRASE.
 GN ASAT5.
 OS Allium tuberosum.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.
 OX NCBI_TaxID=4683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Umano Y., Saito K.,
 RT "Allium tuberosum mRNA for serine acetyltransferase."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB040502; BAA93050.1; -
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 DR Transferrase.
 KW Transferrase.
 SO SEQUENCE 289 AA; 30671 MW; 6DC2D784D25CF383 CRC64;

Query Match 53.1%; Score 872; DB 10; Length 289;
 Best Local Similarity 61.3%; Pred. No. 5.7e-63;
 Matches 166; Conservative 43; Mismatches 62; Indels 0; Gaps 0;

QY 44 DDDVWIKMEAKSDVKOEPIISNTYYASITSHRSLSALAHILSYKLSNLTSLNLF 103
 DB 19 DESWVWQIAEARRADESEPALASLYSTLSSLSLSP 119
 QY 104 ELFTSVLESEPEITESTKODLIAVERDPACISYVHCFEGFGIACQARIATLTKON 163
 DB 79 DFLNMLSTFTTILSKATVADLIAARHDPACIGFSGHLLNFKGFLAVQTORIAHVMSS 138

QY 164 KTVALLIONRSESPAVDHPKAGIKGILLDHTGVIGETAVGDNVSTLHGVTLCG 223
 DB 139 RRELALHRSRADVLSVDHPKAGIKGILLDHTGVIGETAVGDNVSTLHGVTLCG 198
 QY 224 TGKSGDRHPKIGDGVLIAGSCILGNTITGSAKIGSGVYVVDVPARTAVGNPARI 283
 DB 199 TGKAGDRHPKIGDGVLIAGSCILGNTITGSAKIGSGVYVVDVPARTAVGNPARI 258
 QY 284 GKENPKRHKIPCLMDQTSYLETMSDYVI 314
 DB 259 GGEKPKSMHEDVPGESMDHTSFISMSDYII 289

RESULT 7
 O39533 PRELIMINARY; PRT; 294 AA.
 AC O39533;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE SERINE ACETYLTANSFERRASE.
 GN SAT.
 OS Citrullus lanatus (Watermelon) (Citrullus vulgaris).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Cucurbitales; Cucurbitaceae; Citrullus.
 OX NCBI_TaxID=1654;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saito K., Inoue K., Fukushima R., Noji M.,
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-KINRO; TISSUE=GREEN LEAVES.
 RX MEDLINE=95332343; PubMed=7608200;
 RA Saito K., Yokoyama H., Noji M., Murakoshi I.,
 RT "Molecular cloning and characterization of a plant serine
 acetyltransferase playing a regulatory role in cysteine biosynthesis
 from watermelon."
 RT J. Biol. Chem. 270:16321-16326(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KINRO;
 RA Noji M., Inoue K., Saito K.,
 RT Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D85624; BAA12843.1; -
 DR EMBL: D49535; BAA08479.1; -
 DR EMBL: AB006530; BAA21827.1; -
 DR Mendei; 7748; Citla:1221;7748.
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 DR Transferrase.
 KW Transferrase.
 SO SEQUENCE 294 AA; 31537 MW; D9BA9667F638F86D CRC64;

Query Match 53.0%; Score 869; DB 10; Length 294;
 Best Local Similarity 58.6%; Pred. No. 1e-62;
 Matches 163; Conservative 49; Mismatches 66; Indels 0; Gaps 0;

QY 37 IHHTQIEDDDVWIKMEAKSDVKOEPIISNTYYASITSHRSLSALAHILSYKLSN 96
 DB 17 VESTYNNDEFTLWQIKAEARRADESEPALASLYSTLSSLSLSP 119
 QY 97 LPSNTLEFISVLESEPEITESTKODLIAVERDPACISYVHCFEGFGIACQARI 156
 DB 77 LSTLLTLDLEFNAFSTDYCLRSAYVADLQAAERDPACVSHCLNKGFLACQARI 136
 QY 157 HTLMKONKRIYALIONRSESPAVDHPKAGIKGILLDHTGVIGETAVGDNVST 216
 DB 137 HKLMNSRRPLALQSRADVAVDHPKAGIKGILLDHTGVIGETAVGDNVST 196

QY 217 HGVITGCGKSGDRHPRKIGDGLIGAGSCILNITIGEGAKIGSGSVYKVPARTAV 276
 DB 197 HGVITGCGKSGDRHPRKIGDGLIGAGSCILNITIGEGAKIGSGSVYKVPARTAV 256
 QY 277 GNPRLIGKGNPKRHKICITMDOTSTLTMSDYI 314
 DB 257 GNPRLIGKGNPKRHKICITMDOTSTLTMSDYI 294

RESULT 8
 Q9SDP2 PRELIMINARY: PRT: 289 AA.
 AC Q9SDP2;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE SERINE ACETYLTRANSFERASE.
 OS Allium cepa (Onion).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.
 OX NCBI_TaxID=4679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. PUKECOHE LONG KEEPER; TISSUE=ROOT;
 RA Pitter-Joyce M.D., McCallum J.A.;
 RT "Isolation of a serine acetyltransferase cDNA clone from Allium
 cepa."
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF221215; AAF19000.1;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase.
 SQ SEQUENCE 289 AA; 30574 MW; 9EA376C54DA0AF13 CRC64;

Query Match 52.5%; Score 861; DB 10; Length 289;
 Best Local Similarity 59.8%; Pred. No. 4.4e-62;
 Matches 162; Conservative 46; Mismatches 63; Indels 0; Gaps 0;
 QY 44 DDDVVIMKLEAKSDVQOEPLISNYIYASTHSRLESALHILSVKLSNLPSTLFI 103
 DB 19 DESWVWQIKRKAHDESEPALASLYSTILSHPSLARSLSFHLANKLCSSTLSTSLY 78
 QY 104 ELFTSVLESEFEIESTKODLIAVERDPACISYVHCFLGKFLACQAHRIATLMKONR 163
 DB 79 DLFNTLSTPEPTVLSASVADLIAARHRDPACVSHCLNFKGFLAVQIRLAHVLMSOS 138
 QY 164 RKTVALIQRVSESPAVDHPGAKIGKGLLDHATGVVIGETAVGVNDVSLHGVTLGG 223
 DB 139 RRPALALHRSRVDVLSVDHPARIGKGLLDHAGVYIGETAVIGNVSLHHTVTLGG 198
 QY 224 TGQSGDRHPRKIGDGLIGAGSCILNITIGEGAKIGSGSVYKVPARTAVGNPRLI 283
 DB 199 TGAAGDRHPRKIGDGLIGAGATILGNIRIGAGAKVAGSVYLDVPCRTAVGNPRLI 258
 QY 284 GGNENRKHDKPTCLMDOTSTLTMSDYI 314
 DB 259 GGNENRKHDKPTCLMDOTSTLTMSDYI 289

RESULT 9
 Q42538 PRELIMINARY: PRT: 312 AA.
 AC Q42538;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)
 DE (SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SAT-52).
 SAT-52.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 CC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=97201050; PubMed=9048879;
 RA Howarth J.R., Roberts M.A., Wray J.L.;
 RT "Cysteine biosynthesis in higher plants: a new member of the
 Arabidopsis thaliana serine acetyltransferase small gene family
 obtained by functional complementation of an Escherichia coli cysteine
 auxotroph."
 RT Biochim. Biophys. Acta 1350:123-127 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98403864; PubMed=9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT DNA Res. 5:203-216 (1998).
 DR EMBL: U30298; AAC49655.1;
 DR EMBL: AB013392; BAB09894.1;
 DR Mendel: 6699; Arabid. 1221:6699.
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase; Acyltransferase.
 SQ SEQUENCE 312 AA; 32770 MW; 15835510FF31A08 CRC64;

Query Match 51.8%; Score 849.5; DB 10; Length 312;
 Best Local Similarity 59.7%; Pred. No. 4.2e-61;
 Matches 160; Conservative 45; Mismatches 62; Indels 1; Gaps 1;
 QY 48 VWIMLEAKSDVQOEPLISNYIYASTHSRLESALHILSVKLSNLPSTLFI 107
 DB 45 LWTOKKARDAEAEALASLYSTILSHPSLARSLSFHLANKLCSSTLSTSLY 104
 QY 108 SVLESEFEIESTKODLIAVERDPACISYVHCFLGKFLACQAHRIATLMKONR 167
 DB 105 NTFSSDPSLNRATVADLRARVDPACISVSHCLNFKGFLAVQIRLAHVLMSOS 164
 QY 168 ALLIQNVSESPAVDHPGAKIGKGLLDHATGVVIGETAVGVNDVSLHGVTLGG 227
 DB 165 ALALHSRISVFAVDHPGAKIGKGLLDHATGVVIGETAVIGNVSLHHTVTLGG 224
 QY 228 SGRHPRKIGDGLIGAGSCILNITIGEGAKIGSGSVYKVPARTAVGNPRLI 287
 DB 225 CGDRHPRKIGDGLIGAGATILGNIRIGAGAKVAGSVYLDVPCRTAVGNPRLI 284
 QY 288 NPKKHDKPTCLMDOTSTLTMSDYI 314
 DB 285 KPTIHDECCPGESMDTSTLTMSDYI 312

RESULT 10
 Q92PJ4 PRELIMINARY: PRT: 323 AA.
 AC Q92PJ4;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30).
 SAT-106.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OX NCBI_TaxID=3702;
 RN [1]

QY 260 GGSVVYKDYVPARTAVGNPARIIGKENPKRHKDKTICLT 300
 DB 246 AAGSLVKDVPSSHVYVAGNPAKLIRVME-----EQDPSTIAM 281

RESULT 13

Q9JR86 PRELIMINARY; PRT; 272 AA.

AC Q9JR86;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE PUTATIVE SERINE ACETYLTRANSFERASE (EC 2.3.1.30).
 GN CYSE OR NM40742 OR NMB0560.
 OS Neisseria meningitidis (serogroup A), and
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NX NCBI_TaxID=65699, 491.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=2491 / SEROGROUP A / SEROTYPE 4A;
 RC MEDLINE=2022556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 Jagers K., Leather S., Moulé S., Mungall K., Quail M.A.,
 Rajadurai M.A., Rutherford K.M., Simmonds M., Skelton J.,
 Whitehead S., Spratt B.G., Barrall B.G.;
 RT Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491."
 RL Nature 404:502-506(2000).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=MC58 / SEROGROUP B;
 RC MEDLINE=2017575; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,
 Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Ciecko A., Parksey D.S., Blair E., Ciltone J., Clark E.B.,
 Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathevan J.,
 Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58."
 RL Science 287:1809-1815(2000).
 DR EMBL: AL162754; CAB84026.1; -
 DR EMBL: AE002412; AAF40988.1; -
 DR TIGR: NMB0560; -
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase; Acyltransferase.
 SO SEQUENCE 272 AA; 29399 MW; 4CB74DBA916386EB CRC64;

Query Match 39.6%; Score 649.5; DB 2; Length 272;
 Best Local Similarity 50.7%; Pred. No. 5.9e-45;
 Matches 136; Conservative 39; Mismatches 86; Indels 7; Gaps 2;

QY 47 DWIMKLEAKSDVKOEPLISNYIASITSHRSLESALAHILSVKLSINLPSTLFELE 106
 DB 12 LHMHTIRETAFAVSEPMASFLHQTVALRHESGLVLAHLSKIGSPIMDVRLFEIY 71
 QY 107 ISVLESPEITESTKODLAVKERDPACISYVHCFEGFLACQAHRIAHILMKQNKRI 166
 DB 72 QQALGSDTQIGKVEADLKAITEYRDPACDEYSLPLTFEFGFAIDAHRIHNLTYLDGRT 131
 QY 167 VALLIGNRVSEFAVDIHFGAKIGKILLDHAATGVVIGETAVAGNVSTILHGTGTC 226
 DB 132 LAVFLGNRSEVGVVDIHFAARFGYGLMDHATGTAFAGSTAVLGNISSTILHVTIGGSK 191
 QY 227 QSGDRHPKIGDGVLIAGSCIIIGNITIGGAKIGSGVVYKDYVPARTAVGNPARIIGK 286

DB 192 EGGDRHPKIGDGVMIAGNASTILGNIRIGSNNAKIGAGSVVSDVPSITVGVPAKPAVA-- 249
 QY 287 ENPKRHKDKTICLTMDQSTYLTWMSDYVI 314
 DB 250 -----RSKTPSADMONTQTFE-IDFMT 272

RESULT 14

Q9KNT2 PRELIMINARY; PRT; 273 AA.

AC Q9KNT2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE SERINE ACETYLTRANSFERASE.
 GN VC2649.
 OS Vibrio cholerae.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 NX NCBI_TaxID=666;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N1961 / SEROTYPE O1;
 RC MEDLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Ermolaeva L., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 McDonald L., Uitterback T., Fleischmann R.D., Niernan W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae."
 RL Nature 406:477-483(2000).
 DR EMBL: AE004331; AAF95790.1; -
 DR TIGR: VC2649; -
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 4.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase.
 SO SEQUENCE 273 AA; 29278 MW; 5CBEL6376B45B76F CRC64;

Query Match 39.5%; Score 647.5; DB 2; Length 273;
 Best Local Similarity 50.0%; Pred. No. 8.7e-45;
 Matches 132; Conservative 50; Mismatches 71; Indels 11; Gaps 3;

QY 39 HTQLEDDDDVIMKLEAKSDVKOEPLISNYIASITSHRSLESALAHILSVKLSINLP 98
 DB 6 HTK-----VWQTVAEAREQAEQEPMLASFYHATIIKHDSIKKALSYILANRLNTASMP 59
 QY 99 SNTLFELEISVLESPEITESTKODLAVKERDPACISYVHCFEGFLACQAHRIAHIL 158
 DB 60 AMAYREVELEPAADPSISEAACDICTVNRDPVANSYMPLELYLGHYALLOQYRANW 119
 QY 159 LMKQNKRIVALLIGNRVSEFAVDIHFGAKIGKILLDHAATGVVIGETAVAGNVSTILH 218
 DB 120 LMRGRKALATVPQNSIVACQVDIHFAARIGRIMDHAATGTYIGETAVAGNVSTILOD 179
 QY 219 VTLGTGKSGDRHPKIGDGVLIAGSCIIIGNITIGGAKIGSGVVYKDYVPARTAVGN 278
 DB 180 VTLGTGKECGDRHPKIEGVIGAGAKIILGNINIEVGAKIGSGVVLAQVPPHTVAGV 239
 QY 279 PARLIGKENPKRHKDKTICLTMDQ 302
 DB 240 PARTVGRPOS---DK-PSLMDQ 258
 RESULT 15
 Q9SLZ8 PRELIMINARY; PRT; 402 AA.
 ID Q9SLZ8;
 AC Q9SLZ8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
 DE SERINE ACETYLTRANSFERASE.
 GN CMTAT.
 OS Cyanidioschyzon merolae.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.
 OX NCBI_TaxID=45157;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98288115; PubMed=9622597;
 RA Toda K., Takano H., Miyagishi S., Kuroiwa H., Kuroiwa T.;
 RT "Characterization of a chloroplast isoform of serine acetyltransferase
 from the thermo-acidophilic red alga Cyanidioschyzon merolae.";
 RL Biochim. Biophys. Acta 1403:72-84(1998).
 DR EMBL: AB006428; BAA88412.1; -.
 KW Transferase.
 SQ SEQUENCE 402 AA; 43739 MW; D97E69E8FF79F452 CRC64;

Query Match 38.4%; Score 629.5; DB 10; Length 402;
 Best Local Similarity 47.1%; Pred. No. 4.3e-43;
 Matches 130; Conservative 51; Mismatches 92; Indels 3; Gaps 2;

QY 27 FRPGFSVNRKIHHTQIEDDDWIKMLEAKSDVKQEPILSNYYASITSHRSLESALAH 86
 Db 97 FGPVTSVDNW-RTLYSSDPWVELVRREAIGANEPOPLASSLYATVLNHRCTEDTLAF 155
 QY 87 ILVXLSNMLPNSNTLELFISVLESPELIEESTKODLIAVKERDPACISYVHCFLGFG 146
 Db 156 HLANELASPFEOATQYVKLFRDALYQDKSYREAIRADLAVRRDPAMKRCVAVLMYSKG 215
 QY 147 FLACQAHRIAHHTLWKONRKIVALLIONRVSESPAVDIHPGAKIGKGLLDHATGVIGET 206
 Db 216 YALQATRLAHLMRODKVLLALFLOSISKCPAVDIHPARIGSGVMIDHATGIVIGET 275
 QY 207 AVYGDNVSLHGVTLGGTGKQSGDRHPKIGDGVLLIGAGSCILGNITIGEGAKIGSGVVY 266
 Db 276 AVYGNDVSMLANVTLGGTGKQSGDRHPKIGDGVLLIGAGATVIGNIRIGDAQITASSVYL 335
 QY 267 KDVPARTAVGNPARLIGKENPRKHDKIPCLTMDQ 302
 Db 336 KDVPPTIVSGVPAREYKLSYPR--GVYPAFEMDQ 369

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